

FIG. 1A

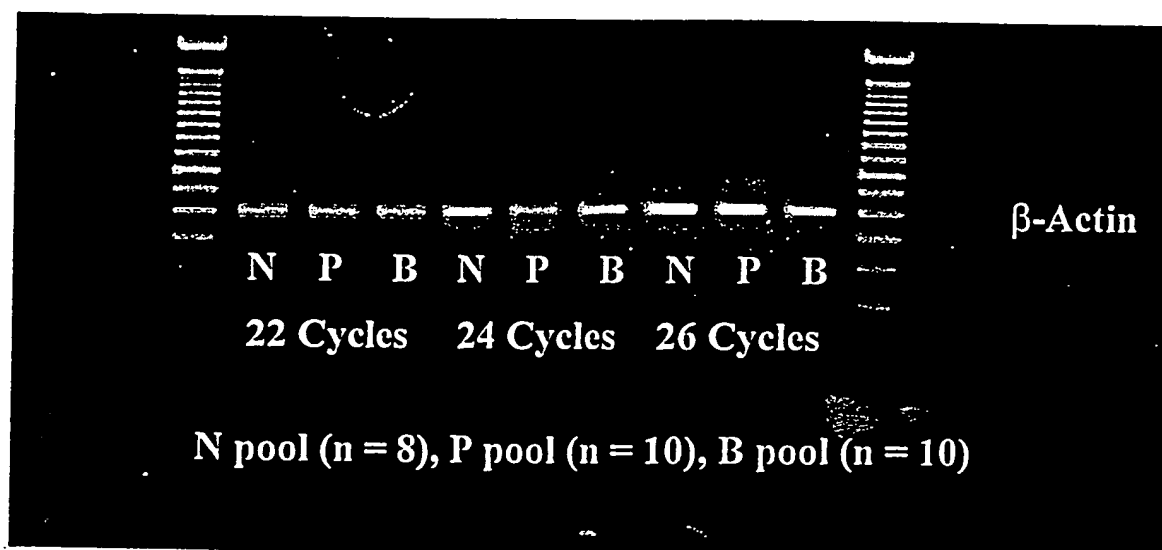


FIG. 1B

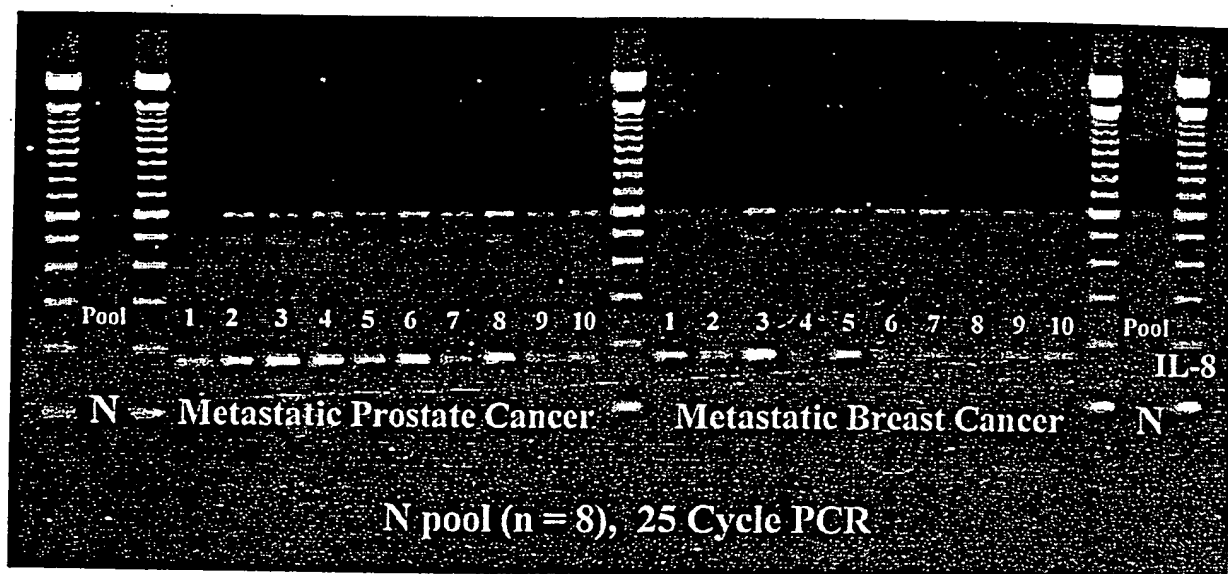


FIG. 2A

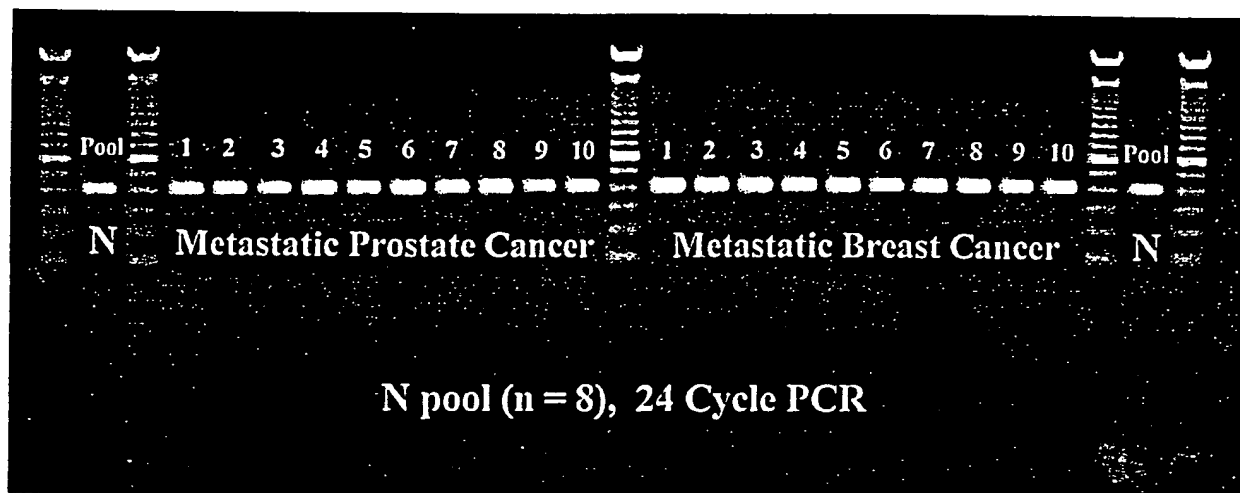


FIG. 2B

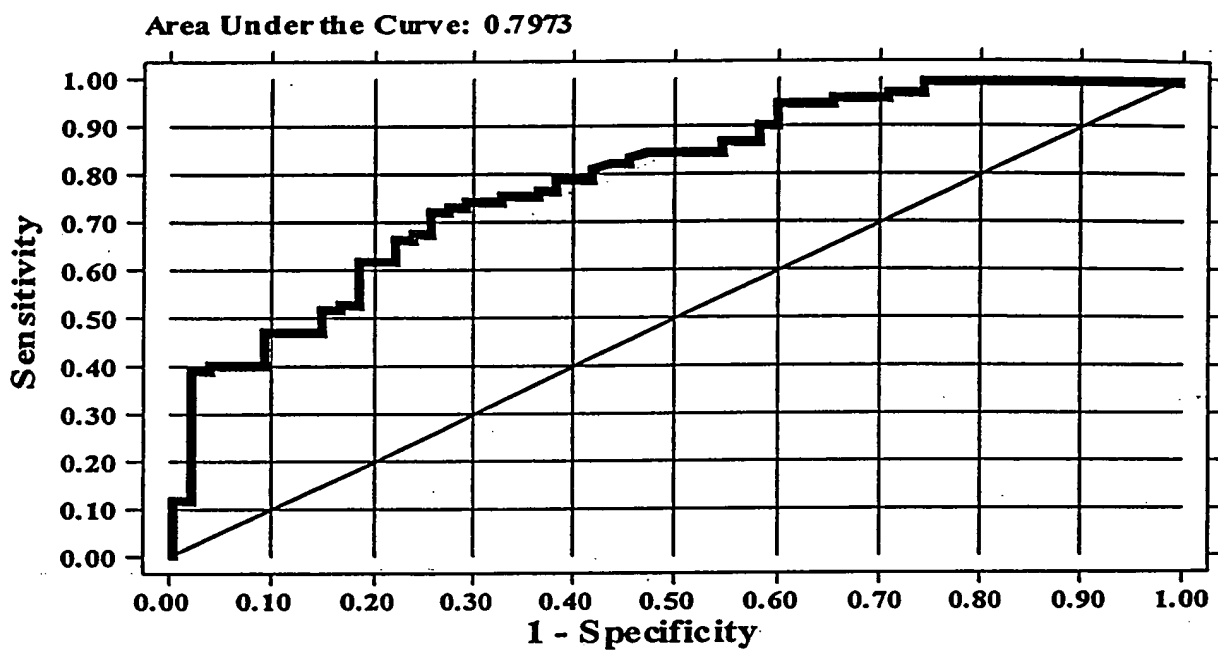


FIG. 3

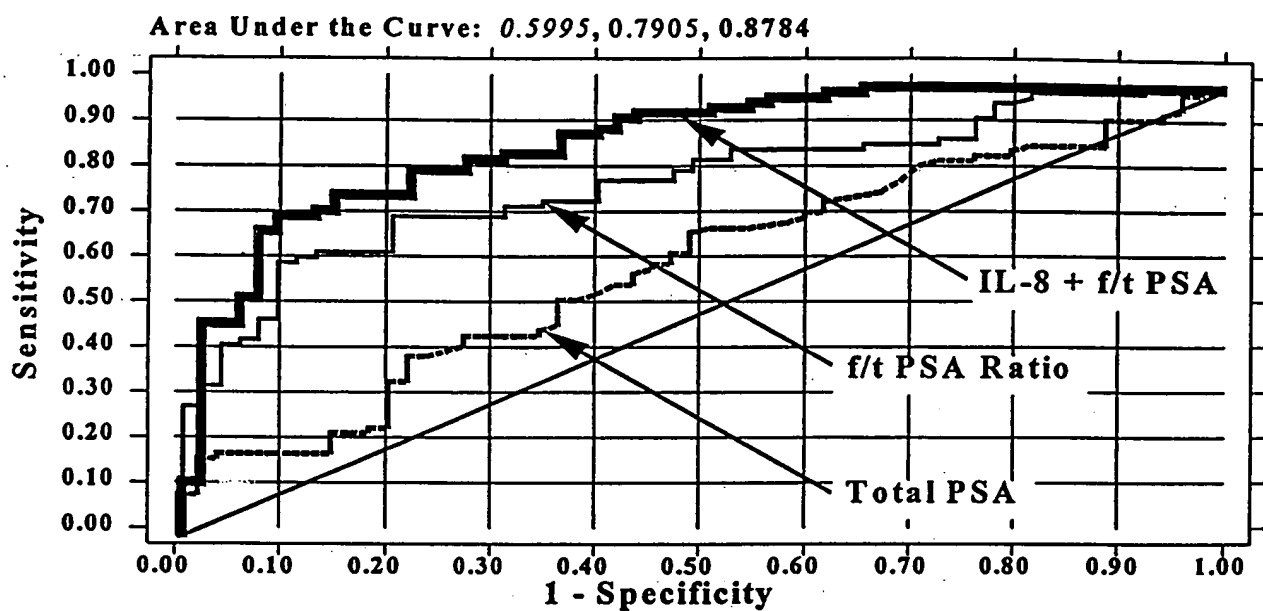
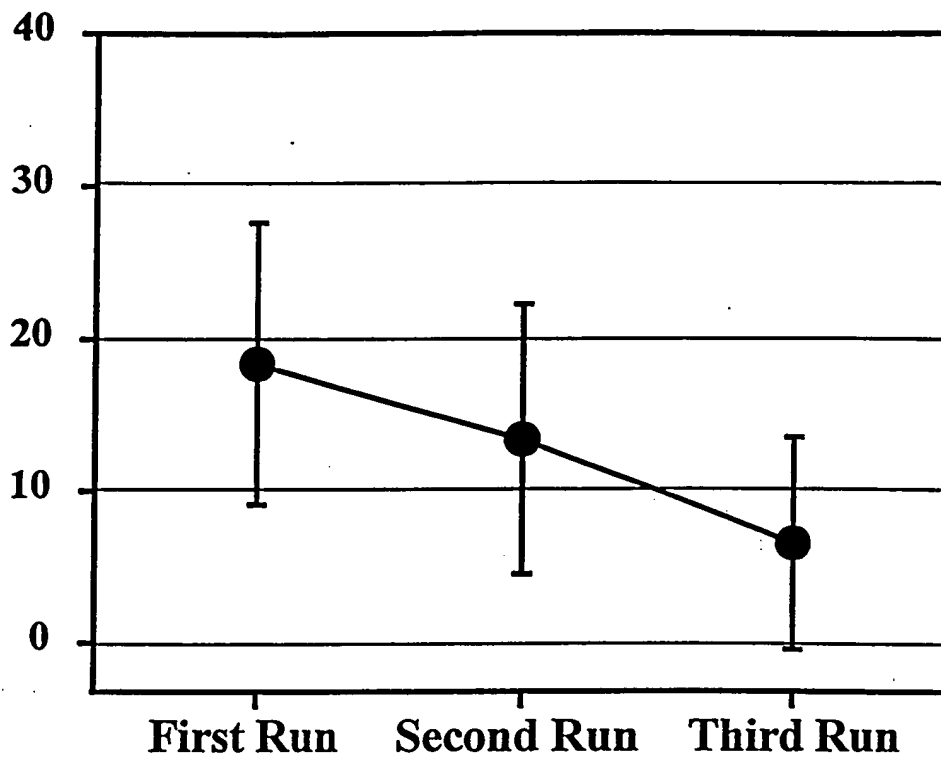


FIG. 4

Average IL-8 (pg/ml)



Freeze/Thaw Sample Sequence

FIG. 5

30	60	
GCGCAGGCGGCAAA	TACGTTGCCGGAGCTGAACGGCGGCTGGTCTGAAGGCAA	HUM-UC331
90	120	
CAAGCGAGCGCGGATAGGGCCGAGAGGACGGCAGGTGGCGGCTTGCCATGTC		HUM-UC331
	START	
150	180	
GCACGGTCACAGCCACGGCGGGGTGGCTGCCGTGCCGCCGACGGGAGGAGCCGCC		HUM-UC331
210	240	
CGAGCAGCGGCCCTGGCCTACGGCCTGTACCTGCGCATCGACCTGGAGCGGCTGCAATG		HUM-UC331
270	300	
CCTTAACGAGAGCCGCGAGGCGGCGCGGCGTCTTCAAGCCATGGGAGGAGCGGAC		HUM-UC331
	TTTCAAGCCGTGGGAGGA - CGGAC	MOU-UC331
	*	*
330	360	
CGACCGCTCCAAGTTATTGAAAGTGATGCAGATGAAGAGCTTCTGTTTAATATTCATT		HUM-UC331
	CGACCGCTCCAAGTTCGCTGAAAGTGATCGGACGGAAGAGCTCCTGTTTAATATTCGTT	MOU-UC331
	*	*
	*	*
390	420	
TACGGGCAATGTCAAGCTCAAAGGCATCATTAATAATGGGAGAGGATGATGACTCACACCC		HUM-UC331
	TACGTGCAATGTCAAGCTGAAAGCGTCAATATAATGGCGAGGATGATGACTCGCACCC	MOU-UC331
	*	*
	*	*

FIG. 6A

CTCTGAGATGAGACTGTACAAGAATAATCCACAGATGTCTTTGATGATACAGAAAGGA	450	480	HUM-UC331
CTCGGAGATGAGACTGTACAAGAACAATCCACAGATGTCAATTTGATGACACAGAAAGGA			MOU-UC331
*	*	*	
GCCAGATCAGACCTTTAGTCTGAACCGGATCTTACAGGAGAAATTAGAGTATGCTACAAA	510	540	HUM-UC331
GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAAATTAGAATATGCTACGAA			MOU-UC331
*	*	*	
AATTCTCGTTTTTCAAATGTCTATCATCTCTCAATTTCATATTTCAAATACTTCGGAGC	570	600	HUM-UC331
AATCTCCAGGTTTTTCAAATGTCTATCATCTTTCCATTTCATATTTCAAATACTTTGGAGC			MOU-UC331
*	*	*	
AGATACGACAAAGTCTTTTATATTGGCCCTGAGAGGAGAGTGGAAGTTCGCCGACA	630	660	HUM-UC331
AGATACGACGAAGATCTTTTATATTGGCCCTGCGGGAGAGTGGAAGTTCGCCGACA			MOU-UC331
*	*	*	
CGAGGTGACCATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATAGGGTCCATCA	690	720	HUM-UC331
TGAGGTGACCATCTGCAACTATGAAGCGTCAGCCAACCCAGCAGACCAACCGGTGCATCA			MOU-UC331
*	*	*	
GGTACCCACAGACACACTTTATTTCTTAAGGGCTGCCAAGGCTCCCATAGAGGCGCT	750	780	HUM-UC331
GGTACCCCGCAGACACACTTTCATTTCTTAAGGGCCAGCCGGGCTCCCTCAGATGCGCT			MOU-UC331
*	*	*	
*STOP	**	**	*

FIG. 6B

810	840
GTGTAGTGAAGATGTACGACTACCTGTTGGGAAGACAAGGATGAGGCTCCAGAGAG	HUM-UC331
GTTAGTGAA--GATGTGCGACCACTGCTGGGAAGGACAGAGG-ATG--CTCCAGCAAT	MOU-UC331
*** ** *	*** ** *
870	900
AGTTGGCTGCCACAGCTCTG-CCAAGCTTTTGTCCTTTGGGGCTTGCTGCAGAAACCTGGCC	HUM-UC331
AGTTGCCCTGCCAGAGCTTTGGCCAGGCTTTGTC-TCGGGG-TTGCTGCAGGAACCTGGCC	MOU-UC331
* * * *	* * *
930	960
TACGGAAGATACGACACCACTGGGAGGTTGTGTAGTGCCAGGGACCATCGTGTTCT	HUM-UC331
TGTGGAACCGCCTCACCAACAGGAGCG--GTATGGGTGCCAAGGA--TAGTCTCTCT	MOU-UC331
** *** ** ** *	*** ** *
990	1020
CTAGGGCGCTGTGGAAATTGGGTCTTTGGGCTGGGTGGCATCTGGCAGTCATGGGTAACAC	HUM-UC331
CTAAGGCACCTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAATGAATAATGC	MOU-UC331
* * * *	** ** *
1050	1080
TTGCTTTTCCAGTTAATGTGGCCCATGTGATTCCAAGTGTCAATGCTTTGTGGAAGATT	HUM-UC331
TCACCTT-CCCAGTC--TGTGGCCACGGGATCCCATGTGCTTTTGTGCTT-GATTTCTTGT	MOU-UC331
** ** *	*** ** *
1110	1140
GTTGTGACTTGTTTTGTGATTTTGTGATTTTGTGTTTAAAGGAACTATTGTGGGC	HUM-UC331
GTGGTTTGTCTT-TTTGTGGCA-----TCAAAAAGGATGCTTCTTGACCG	MOU-UC331
* * * *	*** ** *

FIG. 6C

1170	1200
TATAGGAAACTTCTGATGCCCTCCGGATT-GTGTTAGTAGCCATCAGGAGGTCCTCC	HUM-UC331
TAGAAT--CCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGTCCTCC	MOU-UC331
* * * * *	** ** *
1230	1260
AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTCCCTCTCATTTGTTCAGCATTTCTTGTC	HUM-UC331
AGCTAGAAACACTTCGTCCCTGCTTGCTCCT-CCTCCTGTTCATTGCTCAGCATTCGTGTC	MOU-UC331
* * *	* * *
1290	1320
AAGTTGCCAGCTTGAGTTGTCTGTACGCACATGTGTCTCTGTTATAGCTAGAAGG	HUM-UC331
AGGGTGCCTAGCT-GGTGTACATATCAGACACAAGTGTCCCAATGGTGGTGAAG	MOU-UC331
* * *	* * *
1350	1380
ACAGGAGTCTCCTGCTGATGCGTAGCTTAAGCTTGGGAGAAAGTCTTTTCCACTGC	HUM-UC331
GAAGGAGTCTCCTG--ATACATGACTGCTT-----GGGG--AAGG-CTTACACAGT-C	MOU-UC331
** ** *	** ** *
1410	1440
CTAGCTAAGCAGTCTGGGAGAGCATGGGATCATTTCTATGTGTGGGTAATCTGGTC	HUM-UC331
TAGCCAAATTAGTT--GCGAG-----TCCTTTCCCTGTGT--GGGTGACCTGGTT	MOU-UC331
*** ** *	*** ** *
1470	1500
AG--TAAGATTGAGACTTAGTTAAGATTCCCTTGGAAATTCCTTAATGTTTATTAGCTT	HUM-UC331
GGGGTAAACTGAGACAG--TAAAGATTCCCTTGGGACCTCCTTGGTGTTCCTCGCTT	MOU-UC331
* * *	*** ** *

FIG. 6D

1530

CTAACTAGTGTGTAAGTCCGATGCCAGAAATTGGAGATTGAGTTCTTCTTTTCATGGC HUM-UC331
 CTAACCTCATGTTATAAACCAGGGCTGGAGTCTGGAGACCCCTGCTCCTTCTGTTCATGGC MOU-UC331
 ** * ** ** ** * * * * * *

1560

1590

TTTTATTCACTGTGACTAATAAGCTTCCTAATAAATCCCTTGCCAGACTTAAAAAAA HUM-UC331
 TTTTCATTCAATGAGCTTCCCTAATAAATCCCTTAG-AGACTTAAAA MOU-UC331
 * ** *

1620

* *

10	20	30	40	
MSHGSHGGGCRCAAER-EEPPEQRGLAYGLYLRIDLE				HUM-UC331
>CSHGSHN-----CAAHEIPEVPGDDVYRYDMVSYIDME				ZK353.1

50	60	70	80	
RLQCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF				HUM-UC331
>FKPWEERTDRSKFAESDADEELLF				MOU-UC331
KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF				ZK353.1

90	100	110	120	
NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPQMSFDD				HUM-UC331
NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPQMSFDD				MOU-UC331
NIPFTGHVRLTGLSIIIGDEDGSHPAKIRLFDREAMSFDD				ZK353.1

130	140	150	160	
TEREPDQTFSLNRDLTGELEYATKISRFSNVYHLSIHISK				HUM-UC331
TEREPEQTFSLNRDITGELEYATKISRFSNVYHLSIHISK				MOU-UC331
CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA				ZK353.1

170	180	190	200	
NFGADTTKVIFYIGLRGEWTELRRHEVTICNYEASANPADH				HUM-UC331
NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH				MOU-UC331
NFGEDETKIYYIGLRGEFQHEFRQRIAIATYESRAQLKDH				ZK353.1

210	
RVHQVTPQTHFIS.	HUM-UC331
RVHQVTPQTHFIS.	MOU-UC331
KNEIPDAVAKGLF.	ZK353.1

FIG. 7

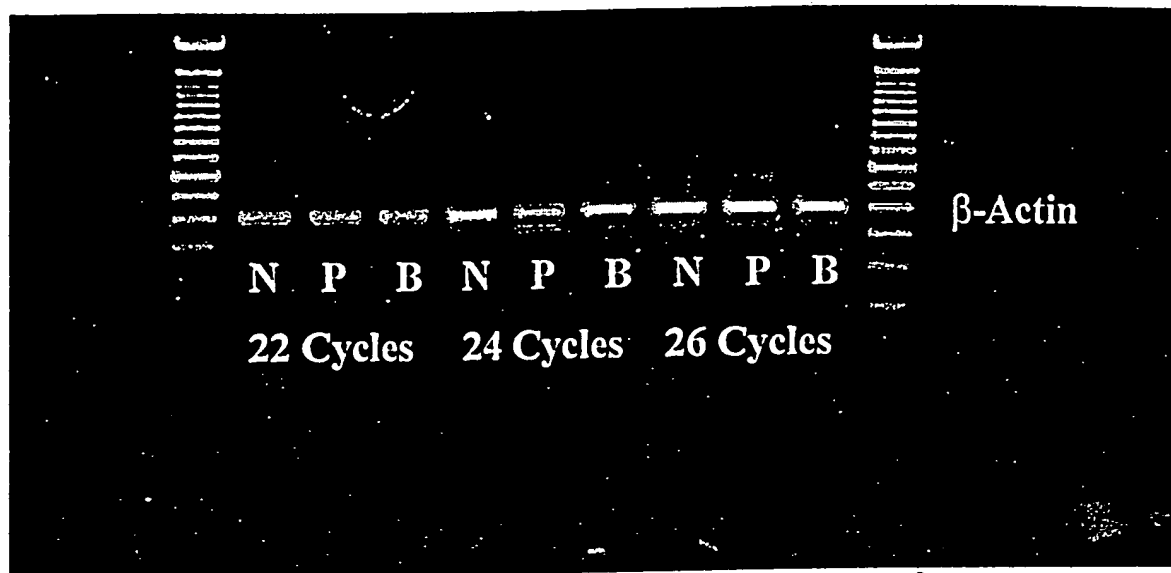
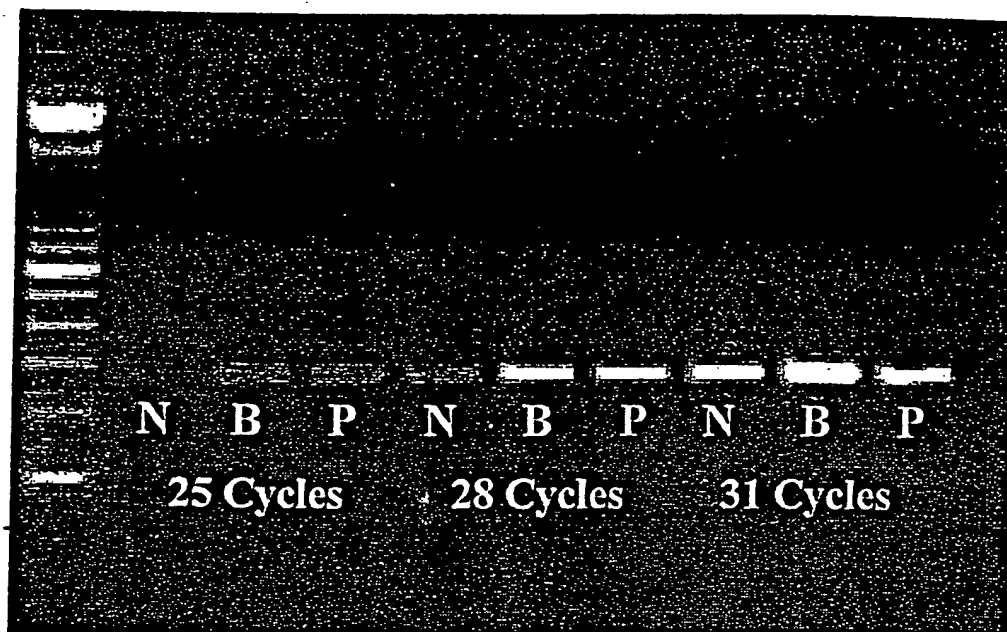


FIG. 8A



UC331

FIG. 8B

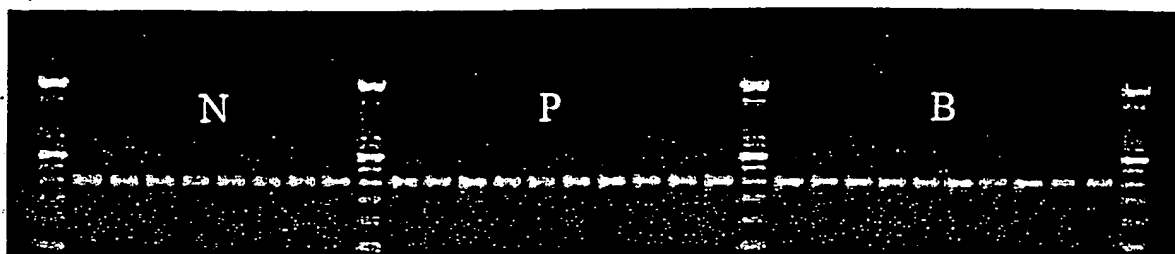


FIG. 9A

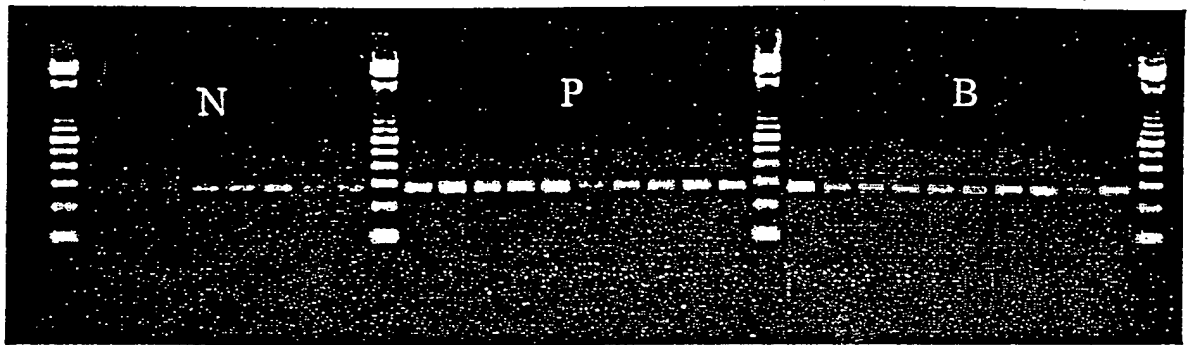


FIG. 9B

1. 1. 1.

10	20	30	40	50
CGACTCGTCG	CCATTCCCGG	AGCAGGTCGG	CCTCGGCCCA	GGGGCGAGTA
60	70	80	90	100
TCCGTTGCTG	TGTCGGAGAC	ACTAGTCCCC	GACACCGAGA	CAGCCAGCCC
110	120	130	140	150
TCTCCCCTGC	CTCGCGGCGG	GAGAGCGTGT	CCGGCCGGCC	GGCCGGCGGG
160	170	180	190	200
GCTCGCGCAA	CCTCCCTCGC	CTCCCCTTCC	CCCGCAGCCT	CCGCCCCGCC
210	220	230	240	250
AGGCCCCGGC	CGGACTCCCG	AGCCCCGGCC	TCCTCGTCCT	CGGTCGCCGC
260	270	280	290	300
TGCCGCCGGG	CTTAACAGCC	CCGTCCGCCG	CTTCTCTTCC	TAGTTTGAGA
310	320	330	340	350
AGCCAAGGAA	GGAAACAGGG	AAAAATGTCG	CCATGAAGGC	CGAGAACCGC
360	370	380	390	400
TGCCGCCGCC	GACCCCCGCC	GGCCCTGAAC	GCCATGAGCC	TGGGTCCCCG
410	420	430	440	450
CCGCGCCCGC	TCCGCTCCGA	CTGCCGTCGC	CGCCGAGGCC	CCCGTTGATG
460	470	480	490	500
CCGCTGAGCT	CCCCCAACGC	CGCCGCCACC	GCCTCCGACA	TGGACAAGAA
510	520	530	540	550
CAGCGGCTCC	AACAGCTCCT	CCGCCTCTTC	GGGCAGCAGC	AAAGGGCAAC
560	570	580	590	600
AGCCGCCCCG	CTCCGCCTCG	GCGGGGCCAG	CCGGCGAGTC	TAAACCCAAG
610	620	630	640	650
AGCGAATTAC	TAATTTACAG	TGGATTCAAT	TTGTTGTCAG	TTGATTCTGT
660	670	680	690	698
AGTAAGGCCA	TATGTTGCCC	CTCTGGAGGT	GCTTGTCAAC	TACTCTGG

ATG	ATG	GAT	GGA	AAG	AAC	TCC	AGT	GGA	TCC	AAG	CGT	TAT	AAT	740
Met	Met	Asp	Gly	Lys	Asn	Ser	Ser	Gly	Ser	Lys	Arg	Tyr	Asn	14

CGC	AAA	CGT	GAA	CTT	TCC	TAC	CCC	AAA	AAT	GAA	AGT	TTT	AAC	782
Arg	Lys	Arg	Glu	Leu	Ser	Tyr	Pro	Lys	Asn	Glu	Ser	Phe	Asn	28

AAC	CAG	TCC	CGT	CGC	TCC	AGT	TCA	CAG	AAA	AGC	AAG	ACT	TTT	824
Asn	Gln	Ser	Arg	Arg	Ser	Ser	Ser	Gln	Lys	Ser	Lys	Thr	Phe	42

AAC	AAG	ATG	CCT	CCT	CAA	AGG	GGC	GGC	GGC	AGC	AGC	AAA	CTC	866
Asn	Lys	Met	Pro	Pro	Gln	Arg	Gly	Gly	Gly	Ser	Ser	Lys	Leu	56

TTT	AGC	TCT	TCT	TTT	AAT	GGT	GGA	AGA	CGA	GAT	GAG	GTA	GCA	908
Phe	Ser	Ser	Ser	Phe	Asn	Gly	Gly	Arg	Arg	Asp	Glu	Val	Ala	70

GAG	GCT	CAA	CGG	GCA	GAG	TTT	AGC	CCT	GCC	CAG	TTC	TCT	GGT	950
Glu	Ala	Gln	Arg	Ala	Glu	Phe	Ser	Pro	Ala	Gln	Phe	Ser	Gly	84

CCT	AAG	AAG	ATC	AAC	CTG	AAC	CAC	TTG	TTG	AAT	TTC	ACT	TTT	992
Pro	Lys	Lys	Ile	Asn	Leu	Asn	His	Leu	Leu	Asn	Phe	Thr	Phe	98

GAA	CCC	CGT	GGC	CAG	ACG	GGT	CAC	TTT	GAA	GGC	AGT	GGA	CAT	1034
Glu	Pro	Arg	Gly	Gln	Thr	Gly	His	Phe	Glu	Gly	Ser	Gly	His	112

FIG. 11A

GGT AGC TGG GGA G AGG AAC AAG TGG GGA CAT A CCT TTT 1076
 Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe 126

AAC AAG GAA CTC TTT TTA CAG GCC AAC TGC CAA TTT GTG GTG 1118
 Asn Lys Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val 140

TCT GAA GAC CAA GAC TAC ACA GCT CAT TTT GCT GAT CCT GAT 1160
 Ser Glu Asp Gln Asp Tyr Thr Ala His Phe Ala Asp Pro Asp 154

ACA TTA GTT AAC TGG GAC TTT GTG GAA CAA GTG CGC ATT TGT 1202
 Thr Leu Val Asn Trp Asp Phe Val Glu Gln Val Arg Ile Cys 168

AGC CAT GAA GTG CCA TCT TGC CCA ATA TGC CTC TAT CCA CCT 1244
 Ser His Glu Val Pro Ser ~~Lys Pro Ile Cys Ser Thr Pro Phe~~ 182

ACT GCA GCC AAG ATA ACC CGT TGT GGA CAC ATC TTC TGC TGG 1286
~~Thr Ala Ala Trp Thr Thr Arg Cys Gly His Ile Phe Cys Thr~~ 196

GCA TGC ATC CTG CAC TAT CTT TCA CTG AGT GAG AAG ACG TGG 1328
~~Val Cys Ile Leu His Tyr Leu Ser Thr Ser Glu Lys Thr Thr~~ 210

AGT AAA TGT CCC ATC TGT TAC AGT TCT GTG CAT AAG AAG GAT 1370
~~Val Lys Cys Pro Ile Cys~~ Tyr Ser Ser Val His Lys Lys Asp 224

CTC AAG AGT GTT GTT GCC ACA GAG TCA CAT CAG TAT GTT GTT 1412
 Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val 238

GGT GAT ACC ATT ACG ATG CAG CTG ATG AAG AGG GAG AAA GGG 1454
 Gly Asp Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly 252

GTG TTG GTG GCT TTG CCC AAA TCC AAA TGG ATG AAT GTA GAC 1496
 Val Leu Val Ala Leu Pro Lys Ser Lys Trp Met Asn Val Asp 266

CAT CCC ATT CAT CTA GGA GAT GAA CAG CAC AGC CAG TAC TCC 1538
 His Pro Ile His Leu Gly Asp Glu Gln His Ser Gln Tyr Ser 280

AAG TTG CTG CTG GCC TCT AAG GAG CAG GTG CTG CAC CGG GTA 1580
 Lys Leu Leu Leu Ala Ser Lys Glu Gln Val Leu His Arg Val 294

GTT CTG GAG GAG AAA GTA GCA CTA GAG CAG CAG CTG GCA GAG 1622
 Val Leu Glu Glu Lys Val Ala Leu Glu Gln Gln Leu Ala Glu 308

GAG AAG CAC ACT CCC GAG TCC TGC TTT ATT GAG GCA GCT ATC 1664
 Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala Ala Ile 322

CAG GAG CTC AAG ACT CGG GAA GAG GCT CTG TCG GGA TTG GCC 1706
 Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala 336

GGA AGC AGA AGG GAG GTC ACT GGT GTT GTG GCT GCT CTG GAA 1748
 Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu 350

FIG. 11B

CAA CTG GTG CTG GCT CCC TTG GCG AAG GAG GTT TTT 1790
 Gln Leu Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe 364

CAA CCC AGG AAG GGT GTG CTG GAG TAT CTG TCT GCC TTC GAT 1832
 Gln Pro Arg Lys Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp 378

GAA GAA ACC ACG GAA GTT TGT TCT CTG GAC ACT CCT TCT AGA 1874
 Glu Glu Thr Thr Glu Val Cys Ser Leu Asp Thr Pro Ser Arg 392

CCT CTT GCT CTC CCT CTG GTA GAA GAG GAG GAA GCA GTG TCT 1916
 Pro Leu Ala Leu Pro Leu Val Glu Glu Glu Glu Ala Val Ser 406

GAA CCA GAG CCT GAG GGG TTG CCA GAG GCC TGT GAT GAC TTG 1958
 Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala Cys Asp Asp Leu 420

GAG TTA GCA GAT GAC AAT CTT AAA GAG GGG ACC ATT TGC ACT 2000
 Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile Cys Thr 434

GAG TCC AGC CAG CAG GAA CCC ATC ACC AAG TCA GGC TTC ACA 2042
 Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr 448

CGC CTC AGC AGC TCT CCT TGT TAC TAC TTT TAC CAA GCG GAA 2084
 Arg Leu Ser Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu 462

GAT GGA CAG CAT ATG TTC CTG CAC CCT GTG AAT GTG CGC TGC 2126
 Asp Gly Gln His Met Phe Leu His Pro Val Asn Val Arg Cys 476

CTC GTG CGG GAG TAC GGC AGC CTG GAG AGG AGC CCC GAG AAG 2168
~~Leu Val Arg Gln Tyr Gly Ser Leu Gln Arg Ser Pro Gln Lys~~ 490

ATC TCA GCA ACT GTG GTG GAG ATT GCT GGC TAC TCC ATG TCT 2210
~~Ile Ser Val Thr Val Val Glu Ile~~ Ala Gly Tyr Ser Met Ser 504

GAG GAT GTT CGA CAG CGT CAC AGA TAT CTC TCT CAC TTG CCA 2252
 Glu Asp Val Arg Gln Arg His Arg Tyr Leu Ser His Leu Pro 518

CTC ACC TGT GAG TTC AGC ATC TGT GAA CTG GCT TTG CAA CCT 2294
 Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu Ala Leu Gln Pro 532

CCT GTG GTC TCT AAG GAA ACC CTA GAG ATG TTC TCA GAT GAC 2336
 Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser Asp Asp 546

ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378
 Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560

GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420
Glu Arg Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574

AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462
 Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

FIG. 11C

CTA CAG CAG TTT C GCC TTC AAT TCT TAT ACC TG CC TCT 2504
 Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602

GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546
 Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616

CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588
 Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630

GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630
 Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644

AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672
 Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658

TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714
 Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672

GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756
 Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686

AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798
 Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700

GAT AAT TCA GAC CGT GTT CCT GTG CCC AGT TTT CAA AAT TCC 2840
 Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714

TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882
 Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728

CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA GGA AAG 2924
 Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Gly Lys 742

AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966
 Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu Phe Ser Thr Ser 756

GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013
 Val Val His Thr Lys Stop 761

TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063

AATTTTAAAG TATTTGAGTT TGAACAGATT AGCTCTGGGG GGAGGGGGTT 3113

TCCACAATGT GAGGGGGAAC CAAGAAAATT TTAAATACAG TGTATTTTCC 3163

AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG 3205

FIG. 11D

C	C		C	H	C	C		C	C	
CPIC	YPPTAAKI	FR	CGHI	ECWAG	EL	HMES	SEK	HSK	CPIC	(UC332)
CPIC	YLPPTAAKI	FR	CDHI	ECWAG	EL	HMES	SEK	HSK	CPIC	(BRCA1)
CPIC	YLPPTAAKI	FR	GNHS	ECRAC	TLNYES	RNTD	KGNC	CPVC		(rpt-1)
CAFCHSV	HNPHQ	IG	CGHR	ECQO	GER	SEREL	NSVPIC	CPVC		(Traf5)
CPIC	MSFIE	QLR	PKLLH	CGHT	ICRQ	CLE	PLASSI	NGVR	CPFC	(HT2A)
CPIC	MSFIE	QLR	PKLLH	CGHT	LOES	CVD	LFVR	HAGN	CEG	(MAT1)
CHVC	QYFAE	PMMLD	CGHN	ICCA	CLA	RCWG	TAE	HNVS	CPQC	(rfp)
GVLC	GGYFID	ATTIE	CLHF	SKTC	IV	RYTE	ISKY	CPIC		(bmi-1)
CAIC	DEYED	GDKLR	ILP	CSHAY	HCK	CVDP	WT	KKTC	CPVC	(CRZF)
CTIC	YENPID	SVLYM	CGHM	CMCY	DCAI	EQWR	GV	GG	CPIC	(neu)

FIG. 12

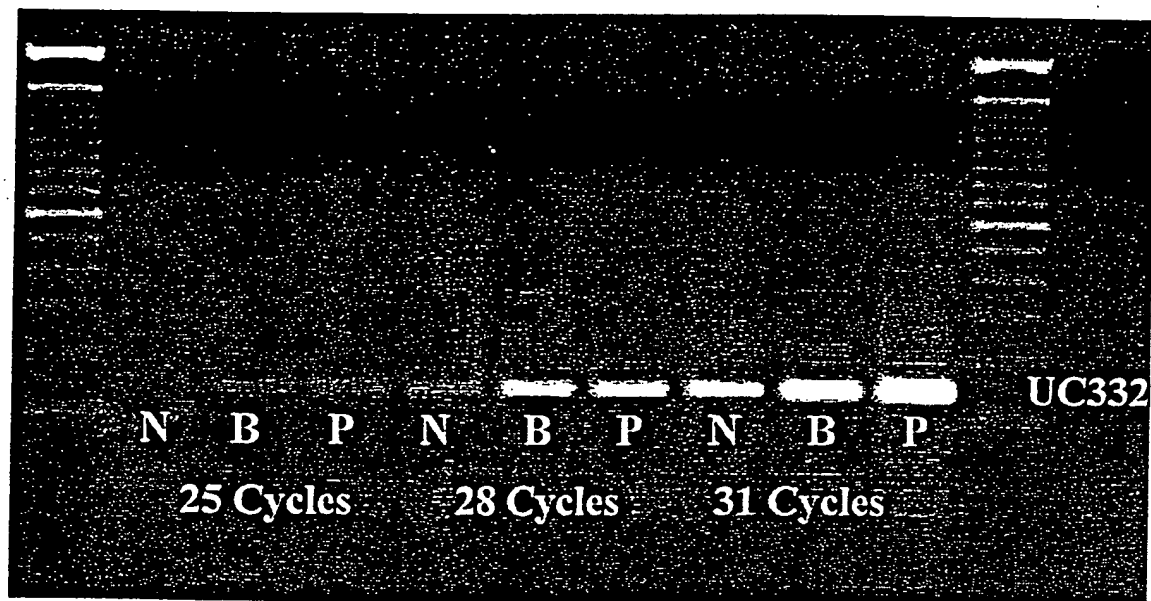


FIG. 13A

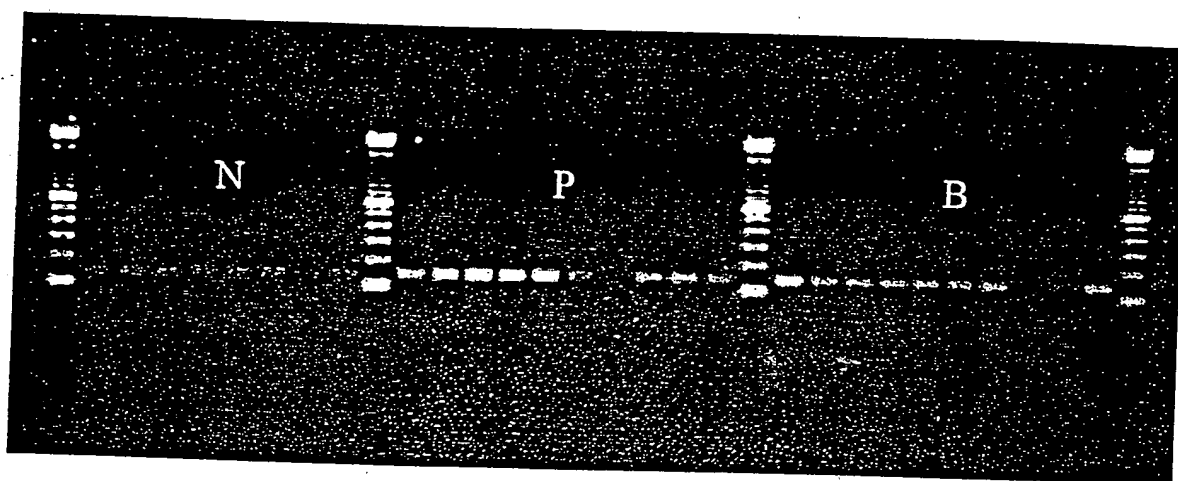


FIG. 13B

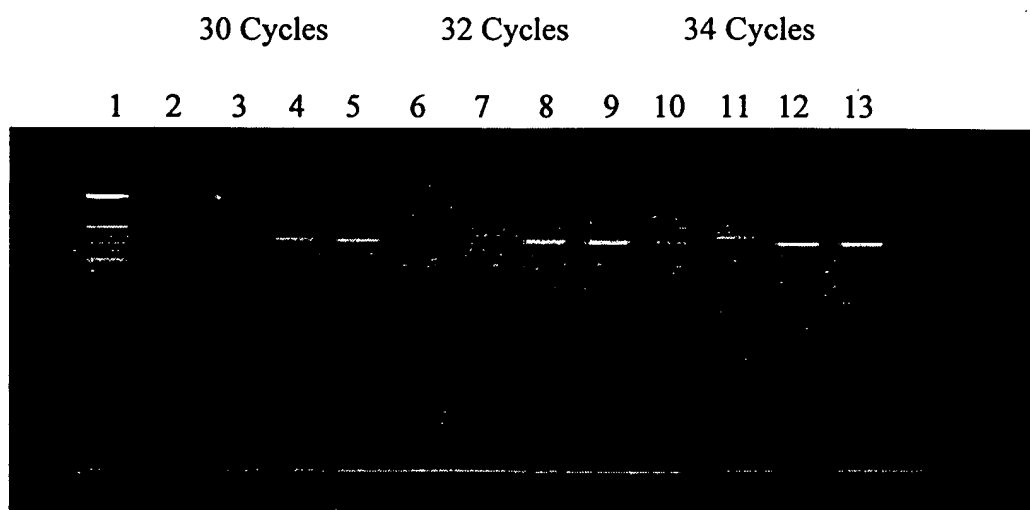


FIG. 14

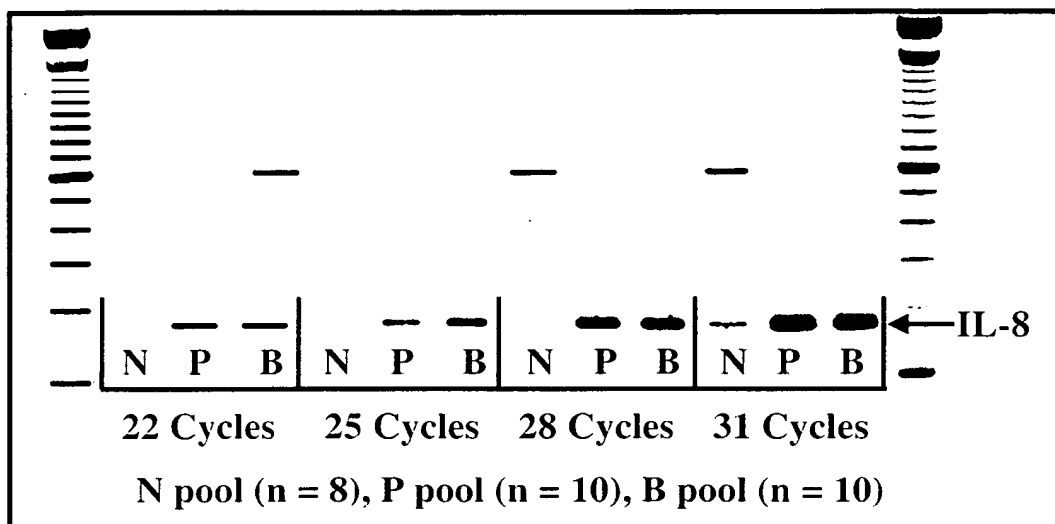


FIG. 1A

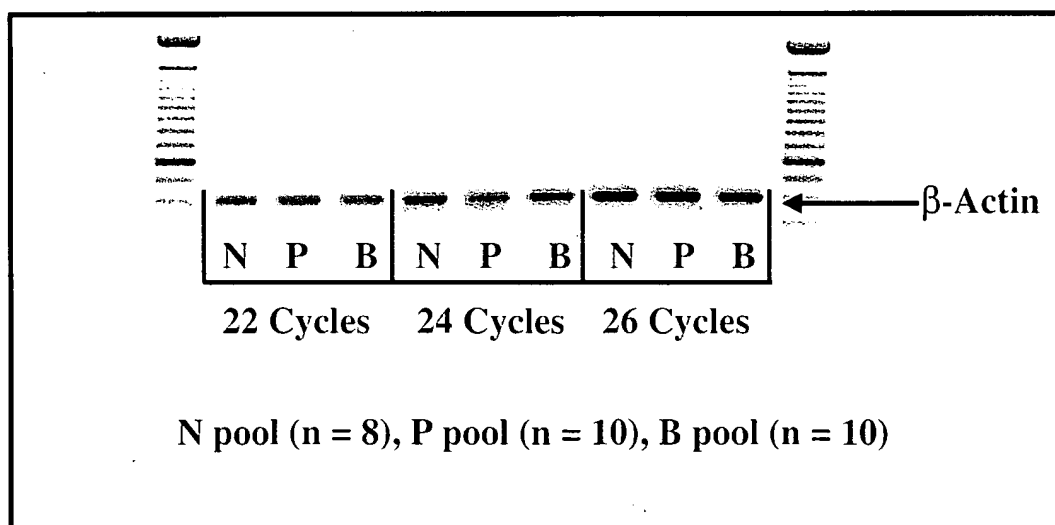


FIG. 1B

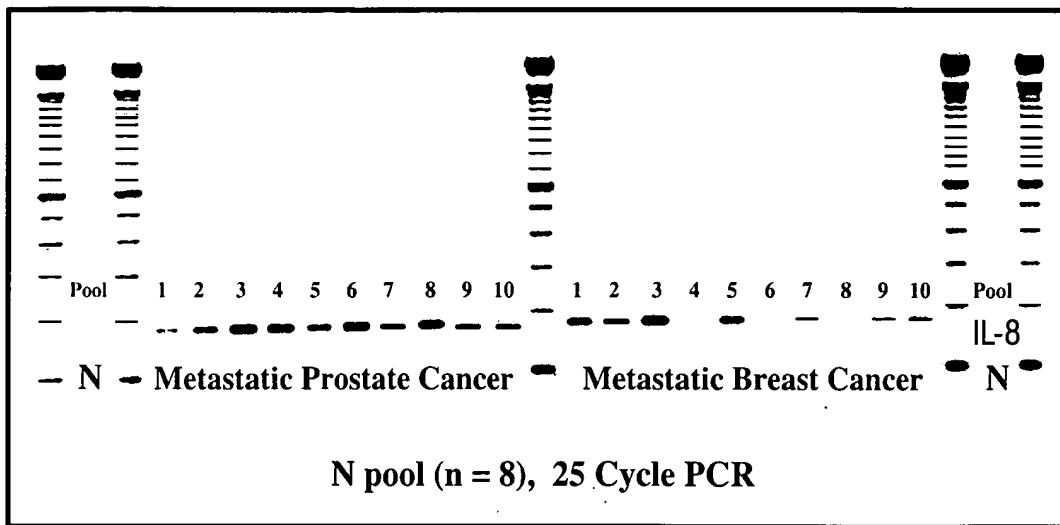


FIG. 2A

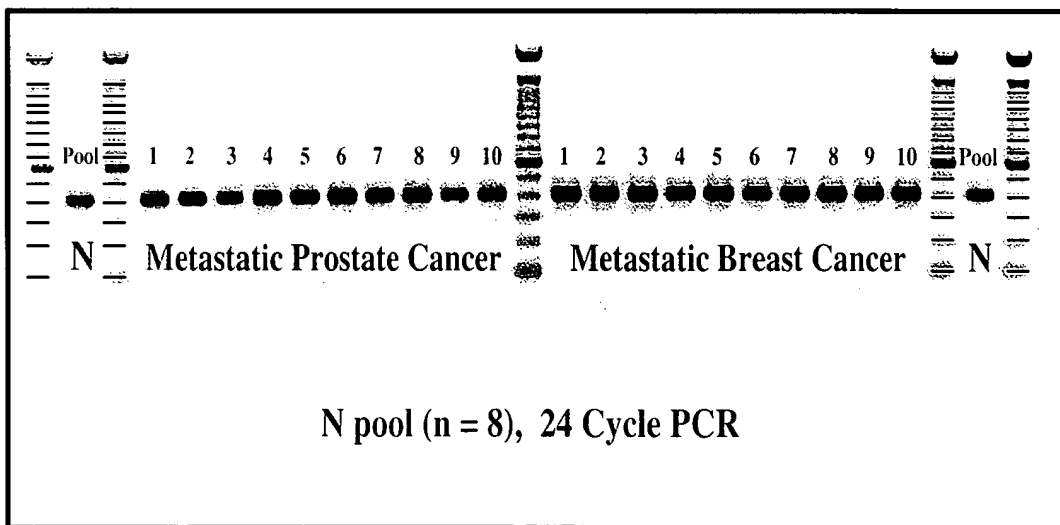


FIG. 2B

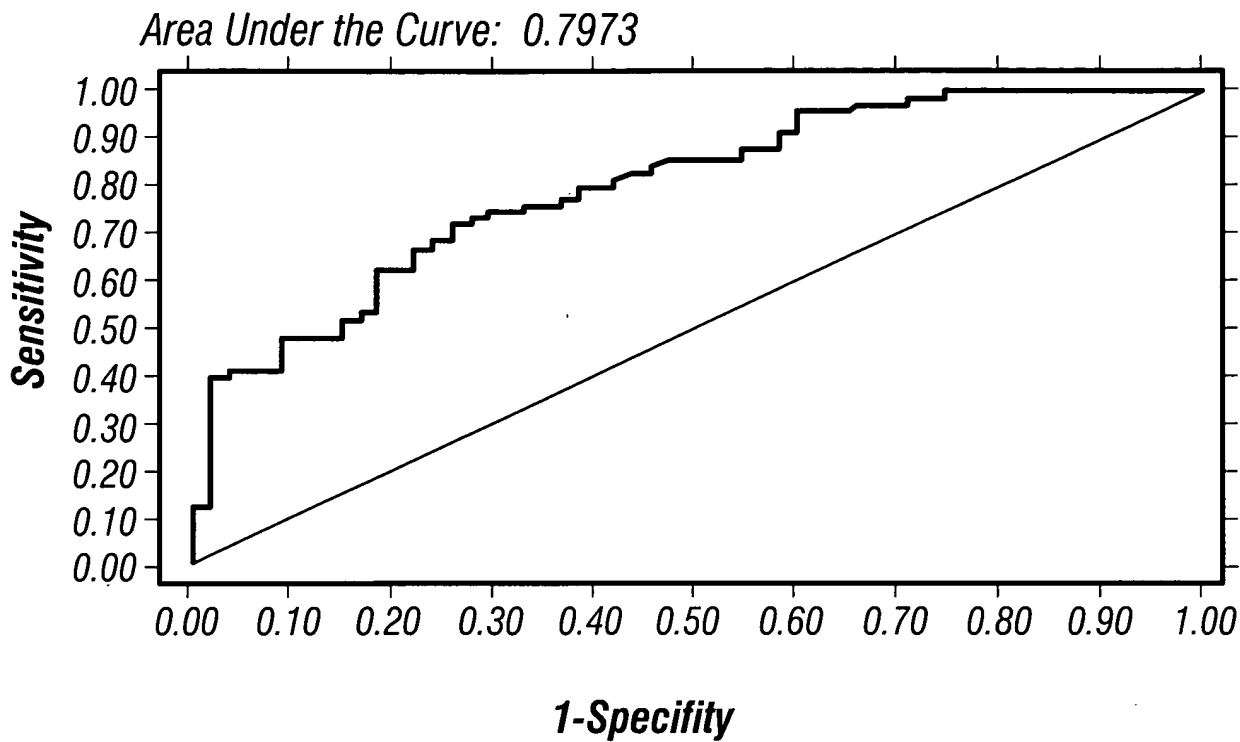


FIG. 3

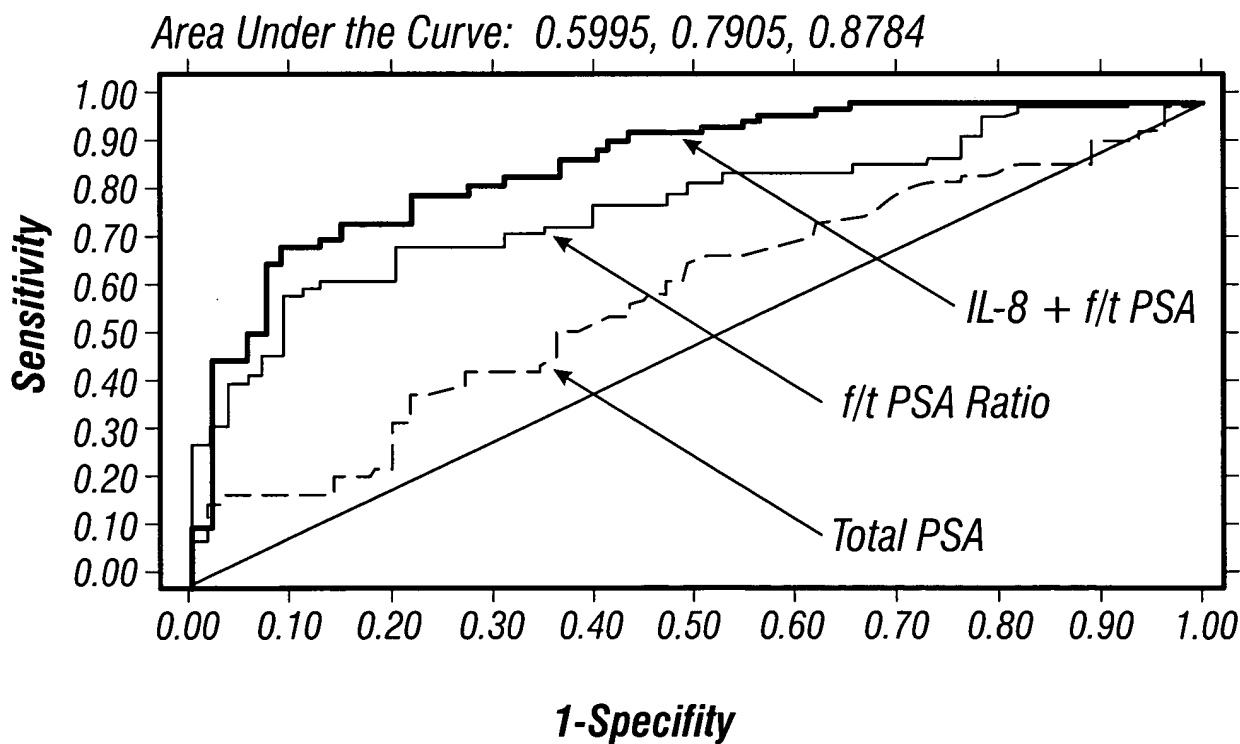


FIG. 4

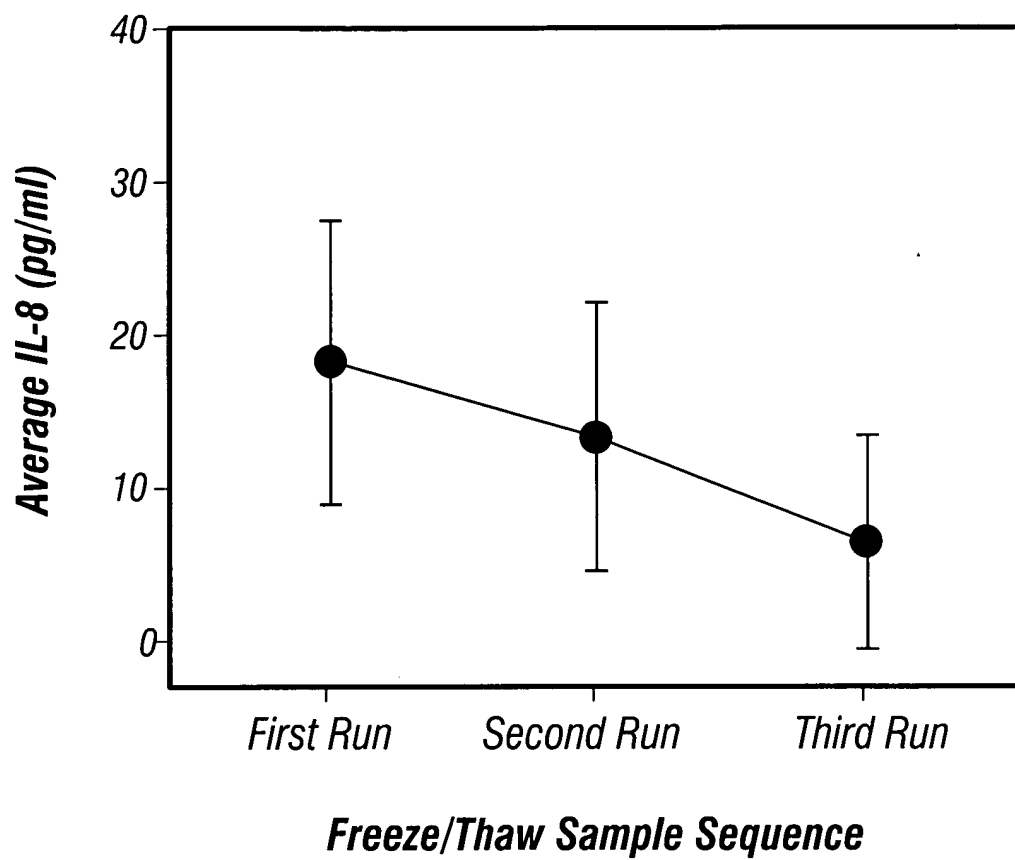


FIG. 5

30	60	
GCGGAGCGCGGCAAAATTACGTTGCCGGAGCTGAACGGCGCGGCTGGTCTGAAGGCAA	HUM-UC331	
90	120	
CAAGCAGCGAGCGCGGATAGGGCGGAGAGGACGCGCAGGTGGCGGCTTGCCATGTC	HUM-UC331	
	START	
150	180	
GCACGGTCACAGCCACGGCGGGGTGGCTGCCGCTGCCGCCGAACGGGAGGAGCCGCC	HUM-UC331	
210	240	
CGAGCAGCGGCGCTACGGCCTGTACCTGCGCATCGACCTGAGCGGCTGCAATG	HUM-UC331	
270	300	
CCTTAACGAGAGCCGCGAGGCGAGCGCGCGGCGTCTTCAAGCCATGGGAGGAGCGGAC	HUM-UC331	
	TTTCAAGCCGTGGGAGGA - CGGAC	MOU-UC331
	*	
330	360	
CGACCGCTCCAAGTTTATTGAAAGTGATGCAGATGAAGAGCTTCTGTTTAATATTCATT	HUM-UC331	
CGACCGCTCCAAGTTCGCTGAAAGTGATGCGGACGAAGAGCTCCTGTTTAATATTCGTT	MOU-UC331	
*	*	*
390	420	
TACGGGCAATGTCAAGCTCAAAGGCATCATTAATAATGGGAGAGGATGATGACTCACACCC	HUM-UC331	
TACGTGCAATGTCAAGCTGAAAGGCGTCATCATAATGGGCGGAGGATGATGACTCGCACCC	MOU-UC331	
*	*	*
450	480	
CTCTGAGATGAGACTGTACAAGAATAATCCACAGATGTCTTGTATGATACAGAAAGGGA	HUM-UC331	
CTCGGAGATGAGACTGTACAAGAACAATCCACAGATGTCTTGTATGATGACACAGAAAGGGA	MOU-UC331	
*	*	*

FIG. 6A

510	540
GCCAGATCAGACCTTTAGTCTGAACCGGATCTTACAGGAAATTAGATGCTACAAA	HUM-UC331
GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAAATTAGAAATATGCTACGAA	MOU-UC331
*	*
570	600
AATTTCGTTTTTCAAATGTCTATCATCTCTCAATTTCATATTTCAAAAAAATTTCGGAGC	HUM-UC331
AATCTCCAGGTTTTTCAAATGTCTATCATCTTTCCATTTCATATTTCAAAAAAATTTCGGAGC	MOU-UC331
* * *	*
630	660
AGATACGACAAAGGTCTTTTATATTTGGCCTGAGAGGAGAGTGGAAGTTCGCCGACA	HUM-UC331
AGATACGACGAAGATCTTTTATATTTGGCCTGCGGGGAGAGTGGAAGTTCGCCGGCA	MOU-UC331
* * *	*
690	720
CGAGGTGACCATCTGCAATTACGAAGCATCTGCCAACCAGCAGACCATAGGGTCCATCA	HUM-UC331
TGAGGTGACCATCTGCAACTATGAAGCGTCAAGCCAGCCAGCAGACCCGGGTGCATCA	MOU-UC331
* * *	*
750	780
GGTTACCCACAGACACACTTTATTTCCCTAAGGGCTGGCCAAGGCTCCCATAGAGCGCT	HUM-UC331
GGTCACCCCGCAGACACACTTTCATTTCTTAAGGGCCAGCCGGGCTCCCTCAGATGCGCT	MOU-UC331
* * *	*
810	840
GTGTCAGTGAAGATGTACGACTACCTGTGTGGGAAGGACAAAGGATGAGGCTCCAGAGAG	HUM-UC331
GTTAGTGAA--GATGTGCAGCACCTGCTGGGAAGGACAGAGG-ATG--CTCCAGCAAT	MOU-UC331
*****	***

FIG. 6B

870	900
AGTTGGCTGCCACAGCTCTG-CCAAGCTTTTGTCTTTTGGGGCTTGCTGCAGAAACCTGGCC	HUM-UC331
AGTTGCCCTGCCAGAGCTTTTGGCCAGGCTTTTGTCTC-TCGGGG-TTGCTGCAGGAACCTGGCC	MOU-UC331
* * * * *	
930	960
TACGGAAGATACGACACCACTGGGAGGGTTGTGTAGTGCCAGGGACCATCGTGGTTCT	HUM-UC331
TGTGGAAACCGCCTCACCAACAGGAGCG--GTATGGGTGCCAAGGGA--TAGTCTCTCT	MOU-UC331
** **** ** ** * * * * *	
990	1020
CTAGGGCGCTGTGGAATTTGGGTCTTTGGGCTGGGTGGCATCTGGCAGTCATGGGTAACAC	HUM-UC331
CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCTCAGTCATGAATAATGC	MOU-UC331
* * * * *	** ** *
1050	1080
TTGCTTTTCCAGTTAATGTGGCCATGTGATTCCAAGTGCATGTGCTTTGTGGAAGATT	HUM-UC331
TCACCT-CCCAGTC--TGTTGGCCACGGGATCCCATGTGTCTTTTGTCTT-GATTCTTGT	MOU-UC331
** ** *	** ** *
1110	1140
GTTGTGACTTGTTTTGTGATTTTGTATTTTGTCTTTTAAAGGAAACTATTGTGGGC	HUM-UC331
GTGGTTGTCTT-TTTGTGGCA-----TCAAAAAGGATGCTTCCTTGACCG	MOU-UC331
* * * * *	** ** *
1170	1200
TATAGGAAACTTCTGATGCCCTCCGGATT-GTGTAGTAGTCCATCAGGAGGTCTCC	HUM-UC331
TAGAAAT--CCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGTCTCC	MOU-UC331
* **** *	** ** *

FIG. 6C

1230	1260
AACTA-AAACACTT-GTTCCTGCTTGCTCCCTTCCCTCTCATTTGTTTCAGCATTTCTTGTC	HUM-UC331
AGCTAGAAACACTTCGTCCTGCTTGCTCCT-CCTCCTGTCATTGCTCAGCATTCGTGTC	MOU-UC331
* * *	*
1290	1320
AAGTTGCCCAGCTTGAGTTGTCTGTACGCACATGTGTCCCTGTGGTTATAGCTAGAAGG	HUM-UC331
AGGGTGCCCTAGCT-GGTGTCACATATCAGACACAAGTGTCCACAAATGGTGGTTGGAAG	MOU-UC331
* * *	*
1350	1380
ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGTCTTTTCCACTGC	HUM-UC331
GAAGGAGTCTCCTG---ATACATGACTGCTT-----GGGG--AAGG-CTTACACAGT-C	MOU-UC331
** * * *	* * * *
1410	1440
CTAGCTAAGCAGTCTGGGAGAGCATGGGATCATTTCTATGTGTGGGTAATCTGGTC	HUM-UC331
TAGCCAAATTAGTT--GCGAG-----TCCTTTCCCTGTGT--GGGTGACCTGGTT	MOU-UC331
*** * *	* * *
1470	1500
AG--TAAGATTGAGACTTAGTTAAGATTCCCCTTGGAATTCCTTAATGTTATTAGCTT	HUM-UC331
GGGTAAAACTGAGACAG--TAAAGATTCCCTCTTGGGACCTCCCTTGGTGTTCCTCCCTGCTT	MOU-UC331
* * *	***
1530	1560
CTAACTAGTGTGTAAGTCCGATGCCAGAAATTTGGAGATTGAGTTCTTCTTTTCATGGC	HUM-UC331
CTAACTCATGTTATAAACCCAGGCTGGAGTCTGGAGACCCCTGCTCCTTCTGTTCATGGC	MOU-UC331
** * *	* * * *

FIG. 6D

Sequence Alignment

1590

1620

TTTTATTCACTGTGACTAATAAGCTTCCTAAATAAATCCTTGCCAGACTTAAAAA AAAA HUM-UC331
TTTCATTCAATGGTGACTAATGAGCTTCCTAAATAAATCCTTAG-AGACTTAAAAA MOU-UC331
* * * *

FIG. 6E

10	20	30	40	
MSHGSHSGGGGCRCAAER- EEPPEQRGLAYGLYLRIDLE				HUM-UC331
>CSHGSHN- - - - -CAAHEIPEVPGDDVYRYDMVSYIDME				ZK353.1
50	60	70	80	
RLQCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF				HUM-UC331
>FKPWEERTDRSKFAESDADEELLF				MOU-UC331
KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF				ZK353.1
90	100	110	120	
NIPFTGNVKLKGIIIMGEDDDSHPSMRLYKNIPQMSFDD				HUM-UC331
NIPFTCNVKLKGVIIMGEDDDSHPSMRLYKNIPQMSFDD				MOU-UC331
NIPFTGHVRLTGLSIIGDEDGSHPAKIRLFDREAMSFDD				ZK353.1
130	140	150	160	
TEREPDQTFSLNRDLTGELEYATKISRFSNVYHLSIHISK				HUM-UC331
TEREPEQTFSLNRDITGELEYATKISRFSNVYHLSIHISK				MOU-UC331
CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA				ZK353.1
170	180	190	200	
NFGADTTKVIFYIGLRGEWTELRRHEVTICNYESANPADH				HUM-UC331
NFGADTTKIFYIGLRGEWTELRRHEVTICNYESANPADH				MOU-UC331
NFGEDETKIYYIGLRGEFQHEFRQRIAIATYESRAQLKDH				ZK353.1
210				
RVHQVTPQTHFIS.				HUM-UC331
RVHQVTPQTHFIS.				MOU-UC331
KNEIPDAVAKGLF.				ZK353.1

FIG. 7

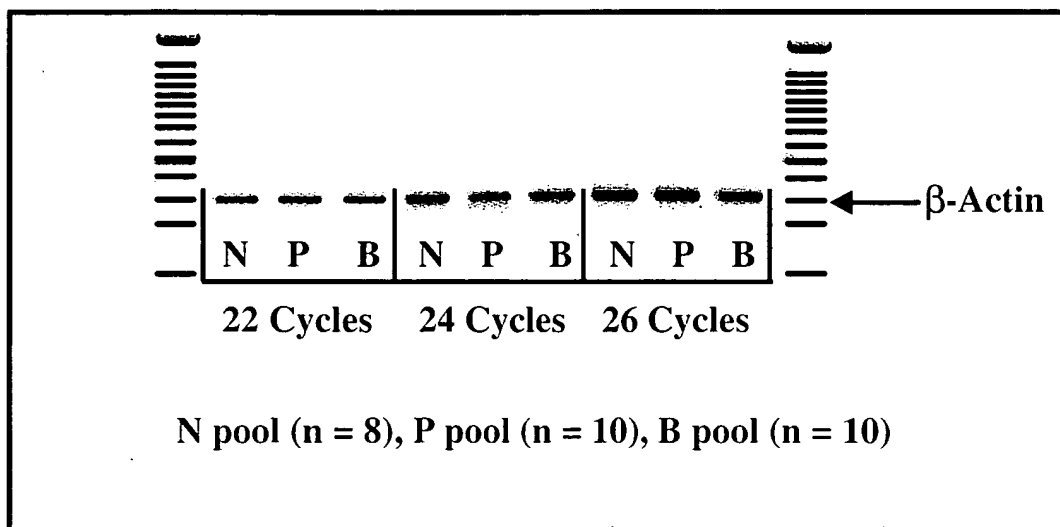


FIG. 8A

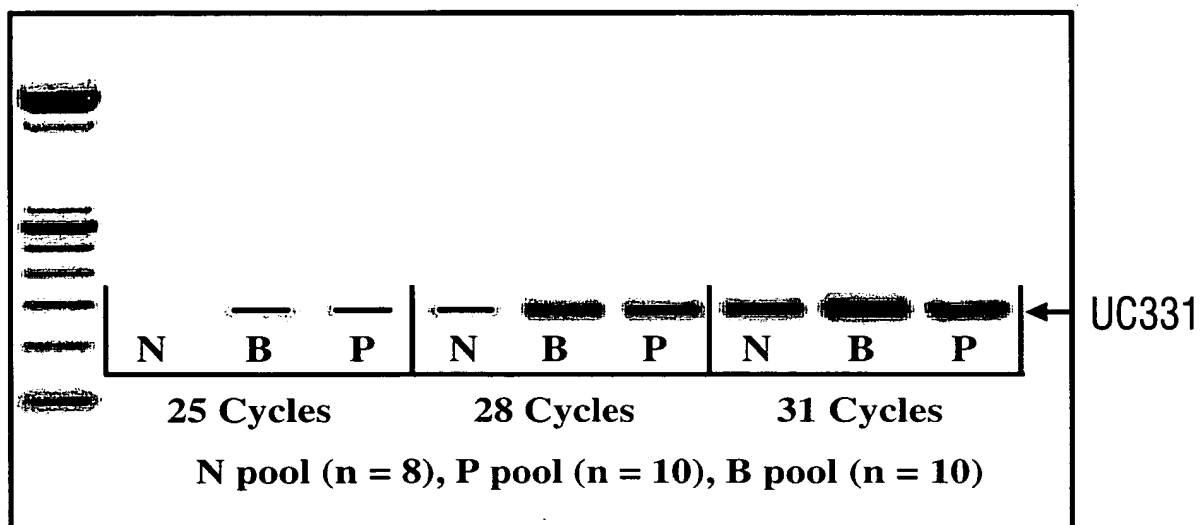


FIG. 8B

Normal Controls										Metastatic Prostate Cancer										Metastatic Breast Cancer									
1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10		

FIG. 9B

Sequence

10	20	30	40	50
CGACTCGTCG	CCATTCCCGG	AGCAGGTCGG	CCTCGGCCCA	GGGCGAGTA
60	70	80	90	100
TCCGTTGCTG	TGTCGGAGAC	ACTAGTCCCC	GACACCGAGA	CAGCCAGCCC
110	120	130	140	150
TCTCCCCCTGC	CTCGGCGCGG	GAGAGCGTGT	CCGGCCGGCC	GGCCGGCGGG
160	170	180	190	200
GCTCGGCGAA	CCTCCCTCGC	CTCCCCCTTC	CCCGCAGCCT	CCGCCCCGCC
210	220	230	240	250
AGGCCCGGCC	CGGACTCCCG	AGCCCCCGCC	TCCTCGTCCT	CGGTCGCCGC
260	270	280	290	300
TGCCGCCGGG	CTTAACAGCC	CCGTCCGCCG	CTTCTCTTCC	TAGTTTGAGA
310	320	330	340	350
AGCCAAGGAA	GGAACACAGG	AAAAATGTGC	CCATGAAGGC	CGAGAACCGC
360	370	380	390	400
TGCCGCCGCC	GACCCCCGCC	GGCCCTGAAC	GCCATGAGCC	TGGGTCCCCG
410	420	430	440	450
CCGCGCCCCG	TCCGCTCCGA	CTGCCGTCGC	CGCCGAGGCC	CCC GTTGATG
460	470	480	490	500
CCGCTGAGCT	CCCCCAACGC	CGCCGCCACC	GCCTCCGACA	TGGACAAGAA
510	520	530	540	550
CAGCGGCTCC	AACAGCTCCT	CCGCCCTCTC	GGGCAGCAGC	AAAGGGCAAC
560	570	580	590	600
AGCCGCCCCG	CTCCGCCCTCG	GCGGGGCCAG	CCGGCGAGTC	TAAACCCAAG

FIG. 11A

610	620	630	640	650
AGCGAATTAC	TAAATTCAGC	TGGATTCAAT	TTGTTGTCAG	TTGATTCTGT
660	670	680	690	698
AGTAAGGCCA	TATGTTGCC	CTCTGGAGGT	GCTTGTCAAC	TACTCTGG
ATG ATG GAT GGA AAG AAC TCC AGT GGA TCC AAG CGT TAT AAT 740				
Met Met Asp Gly Lys Asn Ser Ser Gly Ser Lys Arg Tyr Asn 14				
CGC AAA CGT GAA CTT TCC TAC CCC AAA AAT GAA AGT TTT AAC 782				
Arg Lys Arg Glu Leu Ser Tyr Pro Lys Asn Glu Ser Phe Asn 28				
AAC CAG TCC CGT CGC TCC AGT TCA CAG AAA AGC AAG ACT TTT 824				
Asn Gln Ser Arg Arg Ser Ser Ser Gln Lys Ser Lys Thr Phe 42				
AAC AAG ATG CCT CCT CAA AGG GGC GGC GGC AGC AGC AAA CTC 866				
Asn Lys Met Pro Pro Gln Arg Gly Gly Gly Ser Ser Lys Leu 56				
TTT AGC TCT TCT TTT AAT GGT GGA AGA CGA GAT GAG GTA GCA 908				
Phe Ser Ser Ser Phe Asn Gly Gly Arg Arg Asp Glu Val Ala 70				
GAG GCT CAA CGG GCA GAG TTT AGC CCT GCC CAG TTC TCT GGT 950				
Glu Ala Gln Arg Ala Glu Phe Ser Pro Ala Gln Phe Ser Gly 84				
CCT AAG AAG ATC AAC CTG AAC CAC TTG TTG AAT TTC ACT TTT 992				
Pro Lys Lys Ile Asn Leu Asn His Leu Leu Asn Phe Thr Phe 98				

FIG. 11B

GGT GGA GGC

GAA CCC CGT GGC CAG ACG GGT CAC TTT GAA GGC AGT GGA CAT 1034
Glu Pro Arg Gly Gln Thr Gly His Phe Glu Gly Ser Gly His 112

GGT AGC TGG GGA AAG AGG AAC AAG TGG GGA CAT AAG CCT TTT 1076
Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe 126

AAC AAG GAA CTC TTT TTA CAG GCC AAC TGC CAA TTT GTG GTG 1118
Asn Lys Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val 140

TCT GAA GAC CAA GAC TAC ACA GCT CAT TTT GCT GAT CCT GAT 1160
Ser Glu Asp Gln Asp Tyr Thr Ala His Phe Ala Asp Pro Asp 154

ACA TTA GTT AAC TGG GAC TTT GTG GAA CAA GTG CGC ATT TGT 1202
Thr Leu Val Asn Trp Asp Phe Val Glu Gln Val Arg Ile Cys 168

AGC CAT GAA GTG CCA TCT TGC CCA ATA TGC CTC TAT CCA CCT 1244
Ser His Glu Val Pro Ser Sys Pro Ile Cys Leu Tyr Pro Pro 182

ACT GCA GCC AAG ATA ACC CGT TGT GGA CAC ATC TTC TGC TGG 1286
Thr Ala Ala Lys Ile Thr Arg Cys Gly His Ile Phe Cys Trp 196

GCA TGC ATC CTG CAC TAT CTT TCA CTG AGT GAG AAG ACG TGG 1328
Ala Cys Ile Leu His Tyr Leu Ser Leu Ser Glu Lys Thr Trp 210

FIG. 11C

Sequence

AGT AAA	TGT CCC	ATC TGT	TAC AGT	TCT GTG	CAT AAG	AAG GAT	1370
<u>Ser Lys</u>	<u>Cys Pro</u>	<u>Ile Cys</u>	<u>Tyr Ser</u>	<u>Val Ser</u>	<u>His Lys</u>	<u>Lys Asp</u>	224
CTC AAG	AGT GTT	GCC ACA	GAG TCA	CAT CAG	TAT GTT	GTT Val	1412
Leu Lys	Ser Val	Val Ala	Thr Glu	Ser His	Gln Tyr	Val Val	238
GGT GAT	ACC ATT	ACG ATG	CAG CTG	ATG AAG	AGG GAG	AAA GGG	1454
Gly Asp	Thr Ile	Thr Met	Gln Leu	Met Lys	Arg Glu	Lys Gly	252
GTG TTG	GTG GCT	TTG CCC	AAA TCC	AAA TGG	ATG AAT	GTA GAC	1496
Val Leu	Val Ala	Leu Pro	Lys Ser	Lys Trp	Met Asn	Val Asp	266
CAT CCC	ATT CAT	CTA GGA	GAT GAA	CAG CAC	AGC CAG	TAC TCC	1538
His Pro	Ile His	Leu Gly	Asp Glu	Gln His	Ser Gln	Tyr Ser	280
AAG TTG	CTG CTG	GCC TCT	AAG GAG	CAG GTG	CAC CGG	GTA Val	1580
Lys Leu	Leu Leu	Ala Ser	Lys Glu	Gln Val	Leu His	Arg Val	294
GTT CTG	GAG GAG	AAA GTA	GCA CTA	GAG CAG	CTG GCA	GAG Val	1622
Val Leu	Glu Glu	Lys Val	Ala Leu	Gln Glu	Leu Ala	Glu Glu	308
GAG AAG	CAC ACT	CCC GAG	TCC TGC	TTT ATT	GAG GCA	GCT ATC	1664
Glu Lys	His Thr	Pro Glu	Ser Cys	Phe Ile	Glu Ala	Ile Ile	322

FIG. 11D

TABLE "GGGGG"

CAG	GAG	CTC	AAG	ACT	CGG	GAA	GAG	GCT	CTG	TCG	GGA	TTG	GCC	1706
Gln	Glu	Leu	Lys	Thr	Arg	Glu	Glu	Ala	Leu	Ser	Gly	Leu	Ala	336
GGA	AGC	AGA	AGG	GAG	GTC	ACT	GGT	GTT	GTG	GCT	GCT	CTG	GAA	1748
Gly	Ser	Arg	Arg	Glu	Val	Thr	Gly	Val	Val	Ala	Ala	Leu	Glu	350
CAA	CTG	GTG	CTG	ATG	GCT	CCC	TTG	GCG	AAG	GAG	TCT	GTT	TTT	1790
Gln	Leu	Val	Leu	Met	Ala	Pro	Leu	Ala	Lys	Glu	Ser	Val	Phe	364
CAA	CCC	AGG	AAG	GGT	GTG	CTG	GAG	TAT	CTG	TCT	GCC	TTC	GAT	1832
Gln	Pro	Arg	Lys	Gly	Val	Leu	Glu	Tyr	Leu	Ser	Ala	Phe	Asp	378
GAA	GAA	ACC	ACG	GAA	GTT	TGT	TCT	CTG	GAC	ACT	CCT	TCT	AGA	1874
Glu	Glu	Thr	Thr	Glu	Val	Cys	Ser	Leu	Asp	Thr	Pro	Ser	Arg	392
CCT	CTT	GCT	CTC	CCT	CTG	GTA	GAA	GAG	GAG	GAA	GCA	GTG	TCT	1916
Pro	Leu	Ala	Leu	Pro	Leu	Val	Glu	Glu	Glu	Glu	Ala	Val	Ser	406
GAA	CCA	GAG	CCT	GAG	GGG	TTG	CCA	GAG	GCC	TGT	GAT	GAC	TTG	1958
Glu	Pro	Glu	Pro	Glu	Gly	Leu	Pro	Glu	Ala	Cys	Asp	Asp	Leu	420
GAG	TTA	GCA	GAT	GAC	AAT	CTT	AAA	GAG	GGG	ACC	ATT	TGC	ACT	2000
Glu	Leu	Ala	Asp	Asp	Asn	Leu	Lys	Glu	Gly	Thr	Ile	Cys	Thr	434

FIG. 11E

Genetic Code

GAG	TCC	AGC	CAG	CAG	GAA	CCC	ATC	ACC	AAG	TCA	GGC	TTC	ACA	2042
Glu	Ser	Ser	Gln	Gln	Glu	Pro	Ile	Thr	Lys	Ser	Gly	Phe	Thr	448
CGC	CTC	AGC	AGC	TCT	CCT	TGT	TAC	TAC	TTT	TAC	CAA	GCG	GAA	2084
Arg	Leu	Ser	Ser	Ser	Pro	Cys	Tyr	Tyr	Phe	Tyr	Gln	Ala	Glu	462
GAT	GGA	CAG	CAT	ATG	TTC	CTG	CAC	CCT	GTG	AAT	GTG	CGC	TGC	2126
Asp	Gly	Gln	His	Met	Phe	Leu	His	Pro	Val	Asn	Val	Arg	Cys	476
CTC	GTG	CGG	GAG	TAC	GGC	AGC	CTG	GAG	AGG	AGC	CCC	GAG	AAG	2168
Leu	Val	Arg	Glu	Tyr	Gly	Ser	Leu	Glu	Arg	Ser	Pro	Glu	Lys	490
ATC	TCA	GCA	ACT	GTG	GTG	GAG	ATT	GCT	GGC	TAC	TCC	ATG	TCT	2210
Ile	Ser	Ala	Thr	Val	Val	Glu	Ile	Ala	Gly	Tyr	Ser	Met	Ser	504
GAG	GAT	GTT	CGA	CAG	CGT	CAC	AGA	TAT	CTC	TCT	CAC	TTG	CCA	2252
Glu	Asp	Val	Arg	Gln	Arg	His	Arg	Tyr	Leu	Ser	His	Leu	Pro	518
CTC	ACC	TGT	GAG	TTC	AGC	ATC	TGT	GAA	CTG	GCT	TTG	CAA	CCT	2294
Leu	Thr	Cys	Glu	Phe	Ser	Ile	Cys	Glu	Leu	Ala	Leu	Gln	Pro	532
CCT	GTG	GTC	TCT	AAG	GAA	ACC	CTA	GAG	ATG	TTC	TCA	GAT	GAC	2336
Pro	Val	Val	Ser	Lys	Glu	Thr	Leu	Glu	Met	Phe	Ser	Asp	Asp	546

FIG. 11F

ATT TAA CCG GAG

ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378
 Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560

GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420
Glu Arg Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574

AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462
 Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

CTA CAG CAG TTT CCT GCC TTC AAT TCT TAT ACC TGC TCC TCT 2504
 Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602

GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546
 Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616

CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588
 Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630

GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630
 Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644

AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672
 Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658

FIG. 11G

GenBank

TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714
 Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672

 GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756
 Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686

 AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798
Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700

 GAT AAT TCA GAC CGT GTT CCT CCT GTG CCC AGT TTT CAA AAT TCC 2840
Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714

 TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882
Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728

 CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA AAG 2924
Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Lys 742

 AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966
 Lys Arg Lys Lys Lys Gln Lys Lys Leu Leu Phe Ser Thr Ser 756

 GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013
 Val Val His Thr Lys Stop 761

FIG. 11H

CCF-3333

TGGTTTTGT TTTTGTTTT TTTTCCCCA TGCTTTTGT TGGCTGCTGT 3063
AATTTTAAG TATTGAGTT TGAACACATT AGCTCTGGG GGAGGGGGTT 3113
TCCACAATGT GAGGGGAAC CAAGAAAATT TTAATACAG TGTATTTTCC 3163
AGCTTCCGT CTTACACCA AAATAAGTA TTGACACAAG AG 3205

FIG. 111

Cell Factor

C	C	C	H	C	C	C	C	C	C
CPICLYPPTAAKI	TR	CGHI	FCWACIL	HYLSLEK	TWSK	CPIC	(UC332)		
CPICLELIKEPVSTK		CDHI	FCKFCML	KLLNQKK	SPSQ	CPLC	(BRCA1)		
CPICLELLKEPV	SAD	CNHS	FCRACITLNYE	SNRNTD	GKGN	CPVC	(rpt - 1)		
CAFCHSVLHNPHQTG		CGHR	FCQQCIR	SIRELNSVPI	CPVC		(Traf5)		
CPICMEISFTEE	QLR	PKLLH	ICRQCLE	KLLASSI	NGVR	CPFC	(HT2A)		
CPRCKTTKYRNPSL	KLMVNV	CGHT	LCESCVD	LLFVR	GAGN	CPEC	(MAT1)		
CPVCLQYFAEPMMLD		CGHN	ICACLA	RCWGTAE	TNVS	CPQC	(rfp)		
CVLQGGYFID	ATTIE	CLHF	SCKTCIV	RYLE	TSKY	CPIC	(bmi - 1)		
CAICLDEYEDGDKLRILP		CSHAYHCK	CVDP	WL	TKKT	CPVC	(CRZF)		
CTICYENPIDSVLYM		CGHMC	MYDCAI	EQWRGV	GGG	CPPLC	(neu)		

FIG. 12

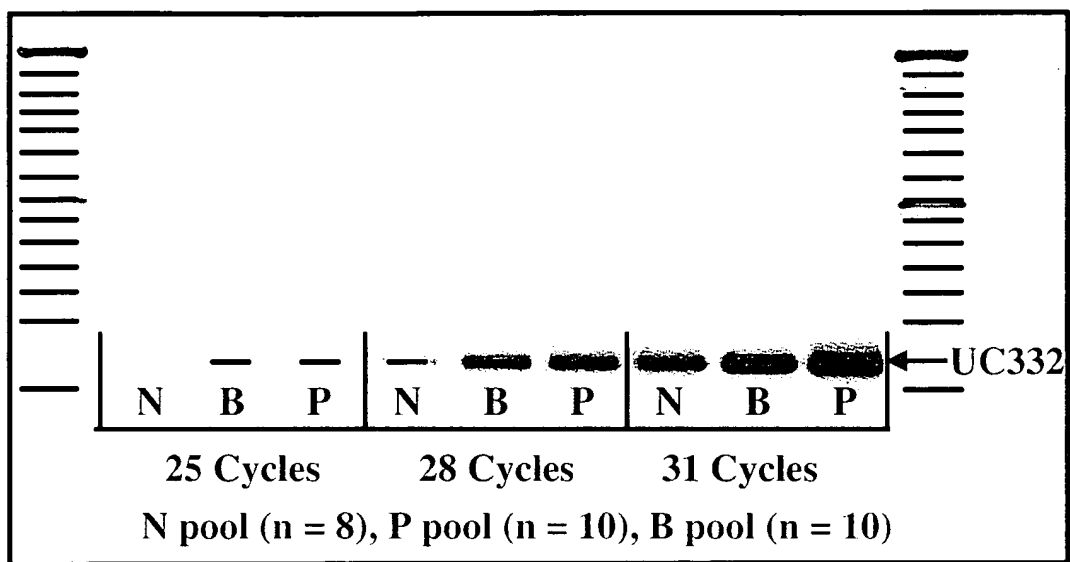


FIG. 13A

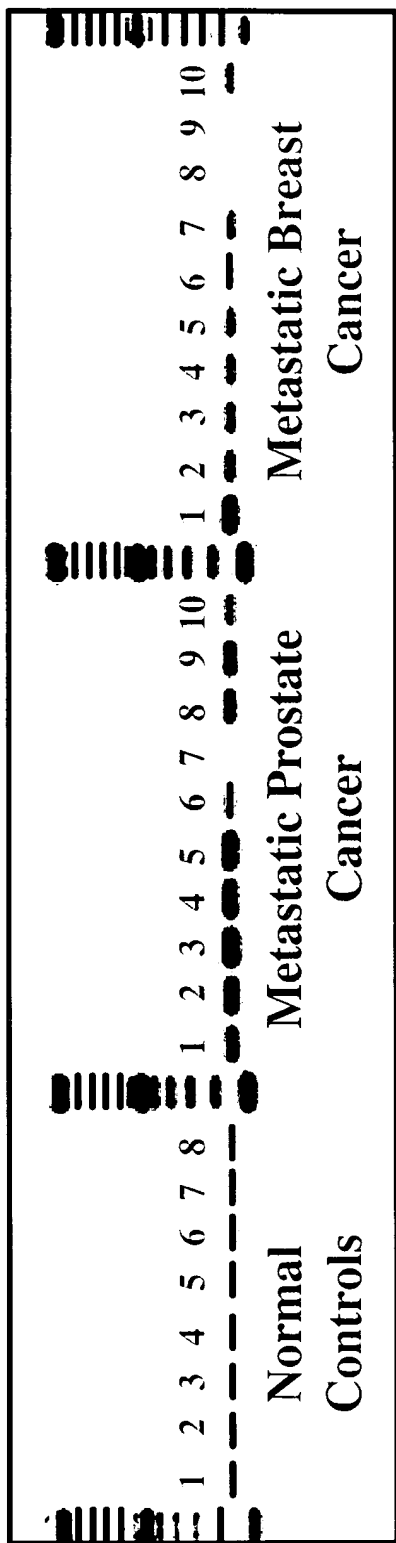


FIG. 13B

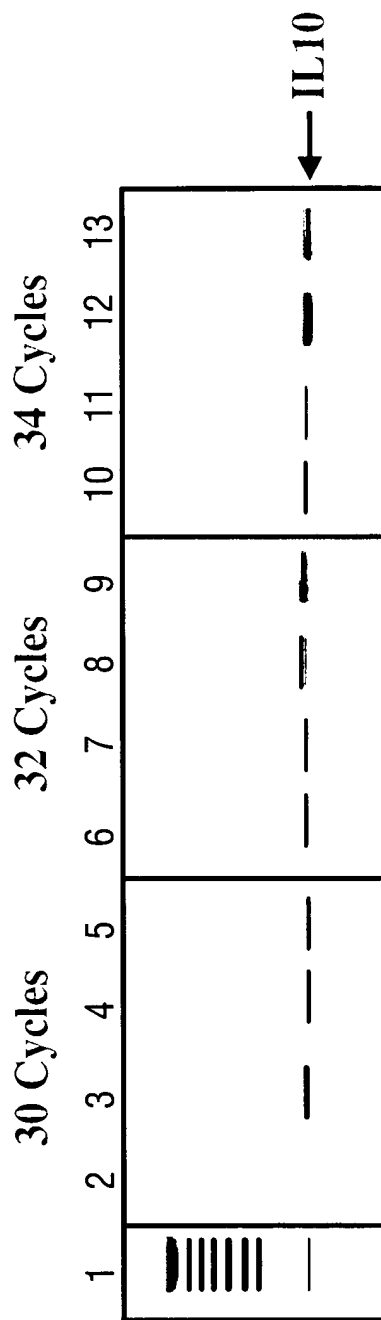


FIG. 14